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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
10/618,852	07/15/2003	Lincoln Muir	IVGN 334	4340
65482	7590	08/24/2007	EXAMINER	
INVITROGEN CORPORATION			NEGIN, RUSSELL SCOTT	
C/O INTELLEVATE				
P.O. BOX 52050			ART UNIT	
MINNEAPOLIS, MN 55402			PAPER NUMBER	
			1631	
			MAIL DATE	
			DELIVERY MODE	
			08/24/2007	
			PAPER	

**Please find below and/or attached an Office communication concerning this application or proceeding.**

The time period for reply, if any, is set in the attached communication.

# Office Action Summary

Application No.

10/618,852

Applicant(s)

MUIR ET AL.

Examiner

Russell S. Negin

Art Unit

1631

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

## Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) OR THIRTY (30) DAYS, WHICHEVER IS LONGER, FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

## Status

- 1) ☒ Responsive to communication(s) filed on 15 March 2007.
- 2a) ☐ This action is FINAL. 2b) ☒ This action is non-final.
- 3) ☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

## Disposition of Claims

- 4) ☒ Claim(s) 37-40 and 42-46 is/are pending in the application.
- 4a) Of the above claim(s) \_\_\_\_\_ is/are withdrawn from consideration.
- 5) ☐ Claim(s) \_\_\_\_\_ is/are allowed.
- 6) ☒ Claim(s) 37-40 and 42-46 is/are rejected.
- 7) ☐ Claim(s) \_\_\_\_\_ is/are objected to.
- 8) ☐ Claim(s) \_\_\_\_\_ are subject to restriction and/or election requirement.

## Application Papers

- 9) ☐ The specification is objected to by the Examiner.
- 10) ☐ The drawing(s) filed on \_\_\_\_\_ is/are: a) ☐ accepted or b) ☐ objected to by the Examiner.  
Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).  
Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).
- 11) ☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

## Priority under 35 U.S.C. § 119

- 12) ☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).
- a) ☐ All b) ☐ Some \* c) ☐ None of:
- ☐ Certified copies of the priority documents have been received.
  - ☐ Certified copies of the priority documents have been received in Application No. \_\_\_\_\_.
  - ☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

\* See the attached detailed Office action for a list of the certified copies not received.

## Attachment(s)

- |  |   |
|--|---|
| 1) <input type="checkbox"/> Notice of References Cited (PTO-892)   | 4) <input type="checkbox"/> Interview Summary (PTO-413)<br>Paper No(s)/Mail Date. _____ |
| 2) <input type="checkbox"/> Notice of Draftsperson's Patent Drawing Review (PTO-948)                       | 5) <input type="checkbox"/> Notice of Informal Patent Application                       |
| 3) <input type="checkbox"/> Information Disclosure Statement(s) (PTO/SB/08)<br>Paper No(s)/Mail Date _____ | 6) <input type="checkbox"/> Other: _____  |

## **DETAILED ACTION**

### ***Comments***

Applicants' amendments and request for reconsideration in the communication filed on 5 June 2007 are acknowledged and the amendments are entered.

Claims 37-40 and 42-46 are pending and examined in the instant Office action.

### ***Sequence Compliance***

In order for the application to be compliant with the sequence rules, applicant must comply with 37 CFR 1.821(f), which states:

(f) In addition to the paper or compact disc copy required by paragraph (c) of this section and the computer readable form required by paragraph (e) of this section, a statement that the "Sequence Listing" content of the paper or compact disc copy and the computer readable copy are the same must be submitted with the computer readable form, e.g., a statement that "the sequence listing information recorded in computer readable form is identical to the written (on paper or compact disc) sequence listing."

In the instant application, there is no such statement in the file.

Additionally, the computer readable form of the sequence listing filed 15 March 2007 was defective. See the attached "Raw Sequence Listing Error Report."

### ***Claim Rejections - 35 USC § 112***

The rejection of claims 37-43 under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which

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applicant regards as the invention is withdrawn in view of the amendments filed on 15 March 2007.

The following is a quotation of the second paragraph of 35 U.S.C. 112:

The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

The following rejection is necessitated by applicant's amendment:

Claim 38 is rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention.

In the phrase "polypeptides are a drugable target," it is unclear as to what is meant by the phrase "drugable target," and how it is differentiated from a target that is not drugable.

### ***Claim Rejections - 35 USC § 102***

The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

A person shall be entitled to a patent unless –

(b) the invention was patented or described in a printed publication in this or a foreign country or in public use or on sale in this country, more than one year prior to the date of application for patent in the United States.

The following rejection is reiterated for claims 37-40 and necessitated by amendment of applicant for claims 44 and 46:

Claims 37-40, 44, and 46 are rejected under 35 U.S.C. 102(e) as being anticipated by Dumas Milne Edwards et al. [USPAT 7,060,479].

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The invention of Dumas Milne Edwards et al., studies full-length human cDNAs encoding potentially secreted proteins and states as its objective on column 4, lines 48-55:

The present invention provides compositions containing a purified or isolated polynucleotide comprising, consisting of, or consisting essentially of a nucleotide sequence selected from the group consisting of: (a) the sequences of SEQ ID Nos: 1-241; (b) the sequences of clone inserts of the deposited clone pool; (c) the full coding sequences of SEQ ID Nos: 1-241; (d) the full coding sequences of the clone inserts of the deposited clone pool; (e) the sequences encoding one of the polypeptides of SEQ ID Nos: 242-482...

Dumas Milne Edwards et al. study the required quantity of clones which encode polypeptides.

Although Dumas Milne Edwards et al. do not explicitly discuss suppressible stop codons, it is inherent in Dumas Milne Edwards et al. that the stop codons discussed are suppressible. Dumas Milne Edwards et al. explain in column 26, lines 39-44 regarding the purpose of stop codons:

Accordingly, the full coding sequence (CDS) or open reading frame (ORF) of each cDNA of the invention refers to the nucleotide sequence beginning with the first nucleotide of the start codon and ending with the last nucleotide of the stop codon.

In the absence of a clear definition in the specification to indicate otherwise, the term "stop codon" is interpreted as a stop codon that can be suppressed. It is an inherent feature for all stop codons that they are suppressible because they at least can be artificially mutated into nonstop codons such that they are suppressed.

Thus, Dumas Milne Edwards et al. describe a clone collection with a size of 241 clones (which fit into the range of about 50 to about 100,000 clones) with suppressible stop codons.

Claim 38 is dependent from claim 37 with the additional limitation that the polypeptides are a drugable target.

Claim 39 is dependent from claim 37 with the additional limitation that the polypeptides are selected from a group of different protein classes.

Claim 40 is dependent from claim 39 where the polypeptides are G-protein-coupled receptors.

Claim 44 is dependent from claim 39 where the polypeptides are kinases.

Consequently, Dumas Milne Edwards et al. discusses clone collections, and they further state in column 301, lines 42-45, "These receptors, which are expressed in the brain, like the protein of the invention, are a novel family of cloned G protein-coupled receptors." G protein-coupled receptors have a finite activity.

In terms of kinases, Dumas Milne Edwards et al. discusses clone collections, and they further state in column 135, lines 56-60, "The EGF receptor, and the related ErbB family of receptor tyrosine kinases, have indeed been much implicated in human cancer."

Many proteins are encoded such that it is interpreted that substantially all of certain species of enzymatic activities are encoded (i.e. G protein coupled receptors and kinases).

Kinases and G-protein coupled receptors are both drugable targets.

Claim 46 is drawn to the same sized clone collection as claim 37 (i.e. from about 50 to about 100,000 clones), each clone comprising in order, a nucleic acid sequence of

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interest, a suppressible stop codon, and a tag sequence wherein the nucleic acid sequence of interest encodes a polypeptide.

The invention of Dumas Milne Edwards et al. studies full-length human cDNAs encoding potentially secreted proteins and states as its objective on column 4, lines 48-55:

The present invention provides compositions containing a purified or isolated polynucleotide comprising, consisting of, or consisting essentially of a nucleotide sequence selected from the group consisting of: (a) the sequences of SEQ ID Nos: 1-241; (b) the sequences of clone inserts of the deposited clone pool; (c) the full coding sequences of SEQ ID Nos: 1-241; (d) the full coding sequences of the clone inserts of the deposited clone pool; (e) the sequences encoding one of the polypeptides of SEQ ID Nos: 242-482...

Consequently, Dumas Milne Edwards et al. study the required quantity of clones which encode polypeptides.

Dumas Milne Edwards et al. continue by discussing in column 152, lines 22-25:

For example, the protein may be rendered easily detectable by inserting the cDNA encoding the protein of the invention into a eukaryotic expression vector in frame with a sequence encoding a tag sequence.

Consequently, Dumas Milne Edwards et al. disclose a method for encoding a protein with a nucleic acid sequence containing a tag sequence.

### ***Claim Rejections - 35 USC § 103***

The rejections of claims 37 and 42 under 35 U.S.C. 103(a) as being unpatentable over Dumas Milne Edwards et al in view of Phillips-Jones et al as applied to claims 37 and 41 above, and further in view of Stearman et al [Science, volume 271, 1996, pages 1552-1557] are withdrawn upon further consideration of the Office.

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The following is a quotation of 35 U.S.C. 103(a) which forms the basis for all obviousness rejections set forth in this Office action:

(a) A patent may not be obtained though the invention is not identically disclosed or described as set forth in section 102 of this title, if the differences between the subject matter sought to be patented and the prior art are such that the subject matter as a whole would have been obvious at the time the invention was made to a person having ordinary skill in the art to which said subject matter pertains. Patentability shall not be negated by the manner in which the invention was made.

This application currently names joint inventors. In considering patentability of the claims under 35 U.S.C. 103(a), the examiner presumes that the subject matter of the various claims was commonly owned at the time any inventions covered therein were made absent any evidence to the contrary. Applicant is advised of the obligation under 37 CFR 1.56 to point out the inventor and invention dates of each claim that was not commonly owned at the time a later invention was made in order for the examiner to consider the applicability of 35 U.S.C. 103(c) and potential 35 U.S.C. 102(e), (f) or (g) prior art under 35 U.S.C. 103(a).

The following 35 U.S.C. 103 Rejections are newly applied:

Claims 42 and 45 are rejected under 35 U.S.C. 103(a) as being unpatentable over Dumas Milne Edwards et al. in view of as applied to claims 37-40, 44, and 46 above, and further in view of Stearman et al. [Science, volume 271, 1996, pages 1552-1557].

Claim 42 is dependent from claim 37 wherein the nucleic acid sequences of interest comprise a tag sequence and the suppressible stop codon is located between the tag sequence and the encoded polypeptide.



Claim 45 is dependent from claim 42 wherein the suppressible stop codon is in-frame with the sequence of interest.

While Dumas Milne Edwards et al. as applied to claims 37-40, 44, and 46 above teach the use of sequences with suppressible stop codons, they do not teach the use of tag sequences in combinations with the suppressible stop codons.

In the article of Stearman et al., Stearman et al. investigates a permease-oxidase complex involved in high-affinity iron uptake in yeast. Stearman et al. describes uses of tags for determining the locations of certain proteins. As stated in the last paragraph of column 2 on page 1554, "We tested this hypothesis by determining the localization of the FTR1 protein, using a MYC epitope-tagged protein." The article continues to describe the use of tags and their insertions in footnote 37 on page 1557.

It would have been obvious at the time of the instant invention to someone of ordinary skill in the art to modify Dumas Milne Edwards et al. as applied to claims 37-40, 44, and 46 in further view of Stearman et al. because Stearman et al. has the advantage of using tags to locate regions of interest which are areas of the sequence which encode desired polypeptides and stop codons. It would have been further obvious to substitute an in-frame suppressible stop codon in the sequence because (in view of the recent decision of KSR International v. Teleflex), a simple substitution of one known element (a suppressible stop codon that is inserted in-frame) to yield a predictable result is a rationale for obviousness.

The following rejection is reiterated from the Office action sent on 18 September 2006:

Claim 43 is rejected under 35 U.S.C. 103(a) as being unpatentable over Dumas Milne Edwards et al. as applied to claims 37-40, 44, and 46 in further view of Senecoff et al. [The Journal of Biological Chemistry, volume 261, 1986, pages 7380-7386].

Claim 43 is dependent from claim 37 with the additional limitation that the nucleic acid sequences of interest are flanked by a first and second recombination site and the first and second recombination sites do not recombine with each other.

Dumas Milne Edwards et al. as applied to claims 37-40, 44, and 46 do not describe the recombination sites as dictated by instant claim 43.

The study of Senecoff et al. studies the directionality in FLP protein-promoted site-specific recombination is mediated by DNA-DNA pairing and illustrates on page 7381, column 1, a double stranded DNA sequence of interest surrounded by two recombination sites. As stated in the first sentence of the abstract, "The 2u plasmid of the yeast *Saccharomyces cerevisiae* encodes a site specific recombination system consisting of plasmid-encoded FLP protein and two recombination sites on the plasmid."

It would have been obvious at the time of the instant invention for someone of ordinary skill in the art to modify Dumas Milne Edwards et al. as applied to claims 37-40, 44, and 46 in view of Senecoff et al. because Senecoff et al. has the ability of using recombination sites to modify sequences for the purposes of understanding directionalities of specific proteins.

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### ***Response to Arguments***

Applicant's arguments filed 15 March 2007 have been fully considered but they are not persuasive.

Applicant has a single argument used to rebut all of the obviousness prior art rejections regarding Dumas Milne Edwards et al. which is stated first on page 10 of the

Remarks of 15 March 2007:

Dumas Milne Edwards et al. discloses a collection of clones which encode proteins which are potentially secreted. Dumas Milne Edwards et al. does not discuss the use of suppressible stop codons and only discusses a clone collection of one specific size, not a range of collection sizes.

This argument is not persuasive because, as claim 37 recites, "a clone collection, comprising: from about 50 to about 100,000 clones." Consequently, a collection of clones ranging between 50 and 100,000 clones is required. The number of clones in the collection of Dumas Milne Edwards et al. is 241, which fits into this range, and consequently can be used to describe the instantly rejected claims.

### ***Conclusion***

No claim is allowed.

Papers related to this application may be submitted to Technical Center 1600 by facsimile transmission. Papers should be faxed to Technical Center 1600 via the central PTO Fax Center. The faxing of such pages must conform with the notices published in the Official Gazette, 1096 OG 30 (November 15, 1988), 1156 OG 61 (November 16, 1993), and 1157 OG 94 (December 28, 1993)(See 37 CFR § 1.6(d)). The Central PTO Fax Center Number is (571) 273-8300.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Russell Negin, Ph.D., whose telephone number is (571) 272-1083. The examiner can normally be reached on Monday-Friday from 7am to 4pm.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's Supervisor, Ram Shukla, Supervisory Patent Examiner, can be reached at (571) 272-0735.

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Information regarding the status of the application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information on the PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free).

*RSN 8/19/07*

RSN  
19 August 2007

/Shubo (Joe) Zhou/  
SHUBO (JOE) ZHOU, PH.D.  
PRIMARY EXAMINER

## **STIC Biotechnology Systems Branch**

### **RAW SEQUENCE LISTING** **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/618,852  
Source: IFW16  
Date Processed by STIC: 3/19/07

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 4.4.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):  
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06.

### Raw Sequence Listing Error Summary

### SUGGESTED CORRECTION

SERIAL NUMBER: 10618,052

**ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE**

- 1 Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino Numbering The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length Sequence(s) \_\_\_\_\_ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) \_\_\_\_\_. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences (OLD RULES) Sequence(s) \_\_\_\_\_ missing. If intentional, please insert the following lines for each skipped sequence:  
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
This sequence is intentionally skipped
- Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences (NEW RULES) Sequence(s) \_\_\_\_\_ missing. If intentional, please insert the following lines for each skipped sequence.  
<210> sequence id number  
<400> sequence id number  
000
- 9 Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.  
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213> Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220> Sequence(s) \_\_\_\_\_ missing the <220> feature and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown". Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n/Xaa "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid



IFW16

## RAW SEQUENCE LISTING

DATE: 03/19/2007

PATENT APPLICATION: US/10/618,852

TIME: 14:33:19

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 5 <120> TITLE OF INVENTION: SUBSCRIPTION BASED SYSTEMS, METHODS AND COMPONENTS FOR PROVIDING

6 GENOMIC AND PROTEOMIC PRODUCTS AND SERVICES

8 &lt;130&gt; FILE REFERENCE: IVGN 334

10 &lt;140&gt; CURRENT APPLICATION NUMBER: 10/618,852

11 &lt;141&gt; CURRENT FILING DATE: 2003-07-15

13 &lt;150&gt; PRIOR APPLICATION NUMBER: 60396241

14 &lt;151&gt; PRIOR FILING DATE: 2002-07-17

16 &lt;160&gt; NUMBER OF SEQ ID NOS: 43

18 &lt;170&gt; SOFTWARE: PatentIn version 3.3

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60

67 cagtattatg tagtctgttt tttatgcaaa atctaattta atatattgat atttatatca

120

Does Not Comply  
 Corrected Diskette Needed  
 (p51-5) @

- What is the  
 source of  
 genetic material?

Invalid  
 Response

- What is the source of genetic  
 material?

Invalid  
 Response

See item #11  
 on error summary  
 sheet.

Same error

Same error

## RAW SEQUENCE LISTING

DATE: 03/19/2007

PATENT APPLICATION: US/10/618,852

TIME: 14:33:19

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132 <210> SEQ ID NO: 9  
133 <211> LENGTH: 27  
134 <212> TYPE: DNA  
135 <213> ORGANISM: Artificial  
137 <220> FEATURE:  
138 <223> OTHER INFORMATION: attB0 *same error*  
140 <400> SEQUENCE: 9  
141 agcctgcttt tttatactaa cttgagc 27  
144 <210> SEQ ID NO: 10  
145 <211> LENGTH: 27



## RAW SEQUENCE LISTING

DATE: 03/19/2007

PATENT APPLICATION: US/10/618,852

TIME: 14:33:19

Input Set : N:\efs\03\_19\_07\10618852\_efs\IVGN334ST25.txt

Output Set: N:\CRF4\03192007\J618852.raw

146 <212> TYPE: DNA  
147 <213> ORGANISM: Artificial  
149 <220> FEATURE:  
150 <223> OTHER INFORMATION: attP0  
152 <400> SEQUENCE: 10  
153 gttcagcttt tttatactaa gttggca  
156 <210> SEQ ID NO: 11  
157 <211> LENGTH: 27  
158 <212> TYPE: DNA  
159 <213> ORGANISM: Artificial  
161 <220> FEATURE:  
162 <223> OTHER INFORMATION: attL0  
164 <400> SEQUENCE: 11  
165 agcctgcttt tttatactaa gttggca  
168 <210> SEQ ID NO: 12  
169 <211> LENGTH: 27  
170 <212> TYPE: DNA  
171 <213> ORGANISM: Artificial  
173 <220> FEATURE:  
174 <223> OTHER INFORMATION: attR0  
176 <400> SEQUENCE: 12  
177 gttcagcttt tttatactaa cttgagc  
180 <210> SEQ ID NO: 13  
181 <211> LENGTH: 27  
182 <212> TYPE: DNA  
183 <213> ORGANISM: Artificial  
185 <220> FEATURE:  
186 <223> OTHER INFORMATION: attP1  
188 <400> SEQUENCE: 13  
189 gttcagcttt tttgtacaaa gttggca  
192 <210> SEQ ID NO: 14  
193 <211> LENGTH: 27  
194 <212> TYPE: DNA  
195 <213> ORGANISM: Artificial  
197 <220> FEATURE:  
198 <223> OTHER INFORMATION: attL1  
200 <400> SEQUENCE: 14  
201 agcctgcttt tttgtacaaa gttggca  
204 <210> SEQ ID NO: 15  
205 <211> LENGTH: 25  
206 <212> TYPE: DNA  
207 <213> ORGANISM: Artificial  
209 <220> FEATURE:  
210 <223> OTHER INFORMATION: attR1  
212 <400> SEQUENCE: 15  
213 gttcagcttt tttgtacaaa cttgt  
216 <210> SEQ ID NO: 16  
217 <211> LENGTH: 25  
218 <212> TYPE: DNA

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Same  
errors

## RAW SEQUENCE LISTING

DATE: 03/19/2007

PATENT APPLICATION: US/10/618,852

TIME: 14:33:19

Input Set : N:\efs\03\_19\_07\10618852\_efs\IVGN334ST25.txt

Output Set: N:\CRF4\03192007\J618852.raw

219 <213> ORGANISM: Artificial  
221 <220> FEATURE:  
222 <223> OTHER INFORMATION: attB2  
224 <400> SEQUENCE: 16  
225 acccagcttt cttgtacaaa gtggt  
228 <210> SEQ ID NO: 17  
229 <211> LENGTH: 27  
230 <212> TYPE: DNA  
231 <213> ORGANISM: Artificial  
233 <220> FEATURE:  
234 <223> OTHER INFORMATION: attP2  
236 <400> SEQUENCE: 17  
237 gttcagcttt cttgtacaaa gttggca  
240 <210> SEQ ID NO: 18  
241 <211> LENGTH: 27  
242 <212> TYPE: DNA  
243 <213> ORGANISM: Artificial  
245 <220> FEATURE:  
246 <223> OTHER INFORMATION: attL2  
248 <400> SEQUENCE: 18  
249 acccagcttt cttgtacaaa gttggca  
252 <210> SEQ ID NO: 19  
253 <211> LENGTH: 25  
254 <212> TYPE: DNA  
255 <213> ORGANISM: Artificial  
257 <220> FEATURE:  
258 <223> OTHER INFORMATION: attr2  
260 <400> SEQUENCE: 19  
261 gttcagcttt cttgtacaaa gtggt  
264 <210> SEQ ID NO: 20  
265 <211> LENGTH: 22  
266 <212> TYPE: DNA  
267 <213> ORGANISM: Artificial  
269 <220> FEATURE:  
270 <223> OTHER INFORMATION: attB5  
272 <400> SEQUENCE: 20  
273 caactttatt atacaaagtt gt  
276 <210> SEQ ID NO: 21  
277 <211> LENGTH: 27  
278 <212> TYPE: DNA  
279 <213> ORGANISM: Artificial  
281 <220> FEATURE:  
282 <223> OTHER INFORMATION: attP5  
284 <400> SEQUENCE: 21  
285 gttcaacttt attatacaaaa gttggca  
288 <210> SEQ ID NO: 22  
289 <211> LENGTH: 24  
290 <212> TYPE: DNA  
291 <213> ORGANISM: Artificial

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*Same  
errors*

## RAW SEQUENCE LISTING

DATE: 03/19/2007

PATENT APPLICATION: US/10/618,852

TIME: 14:33:19

Input Set : N:\efs\03\_19\_07\10618852\_efs\IVGN334ST25.txt

Output Set: N:\CRF4\03192007\J618852.raw

293 <220> FEATURE:  
294 <223> OTHER INFORMATION: attL5  
296 <400> SEQUENCE: 22  
297 caactttatt atacaaagtt ggca  
300 <210> SEQ ID NO: 23  
301 <211> LENGTH: 25  
302 <212> TYPE: DNA  
303 <213> ORGANISM: Artificial  
305 <220> FEATURE:  
306 <223> OTHER INFORMATION: attr5  
308 <400> SEQUENCE: 23  
309 gttcaacttt attatacaaa gttgt  
312 <210> SEQ ID NO: 24  
313 <211> LENGTH: 22  
314 <212> TYPE: DNA  
315 <213> ORGANISM: Artificial  
317 <220> FEATURE:  
318 <223> OTHER INFORMATION: attB11  
320 <400> SEQUENCE: 24  
321 caacttttct atacaaagtt gt  
324 <210> SEQ ID NO: 25  
325 <211> LENGTH: 27  
326 <212> TYPE: DNA  
327 <213> ORGANISM: Artificial  
329 <220> FEATURE:  
330 <223> OTHER INFORMATION: attP11  
332 <400> SEQUENCE: 25  
333 gttcaacttt tctatacaaa gttggca  
336 <210> SEQ ID NO: 26  
337 <211> LENGTH: 24  
338 <212> TYPE: DNA  
339 <213> ORGANISM: Artificial  
341 <220> FEATURE:  
342 <223> OTHER INFORMATION: attL11  
344 <400> SEQUENCE: 26  
345 caacttttct atacaaagtt ggca  
348 <210> SEQ ID NO: 27  
349 <211> LENGTH: 25  
350 <212> TYPE: DNA  
351 <213> ORGANISM: Artificial  
353 <220> FEATURE:  
354 <223> OTHER INFORMATION: attr11  
356 <400> SEQUENCE: 27  
357 gttcaacttt tctatacaaa gttgt  
360 <210> SEQ ID NO: 28  
361 <211> LENGTH: 22  
362 <212> TYPE: DNA  
363 <213> ORGANISM: Artificial  
365 <220> FEATURE:

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Same  
errors

See item

# 11 on

error  
summary  
sheet

The type of errors shown exist throughout  
the Sequence Listing. Please check subsequent  
sequences for similar errors.

RAW SEQUENCE LISTING ERROR SUMMARY      DATE: 03/19/2007  
PATENT APPLICATION: US/10/618,852      TIME: 14:33:20

Input Set : N:\efs\03\_19\_07\10618852\_efs\IVGN334ST25.txt  
Output Set: N:\CRF4\03192007\J618852.raw

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,  
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:1,2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22,23,24,25,26,27

Seq#:28,29,30,31,32,33,34,35,36,37,38,39,40,41,42,43

**VERIFICATION SUMMARY**

DATE: 03/19/2007

PATENT APPLICATION: US/10/618,852

TIME: 14:33:20

Input Set : N:\efs\03\_19\_07\10618852\_efs\IVGN334ST25.txt

Output Set: N:\CRF4\03192007\J618852.raw